

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:22:07 ; Search time 88.16 seconds
(without alignments)
27.919 Million cell updates/sec

Title: US-09-331-631A-38

Perfect score: 53
Sequence: 1 CXXXXXXXXXXXXXXCXXC 21

Scoring table: BLOSUM62PX
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_FODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	32	6	077490
2	53	100.0	32	6	077493
3	53	100.0	46	4	016861
4	53	100.0	58	5	090623
5	53	100.0	62	10	09M402
6	53	100.0	66	12	041097
7	53	100.0	72	5	09V199
8	53	100.0	73	5	062554
9	53	100.0	73	5	062555
10	53	100.0	74	5	09V1A1
11	53	100.0	74	6	09N0X1
12	53	100.0	81	4	016274
13	53	100.0	83	11	09JM45
14	53	100.0	84	12	072913
15	53	100.0	84	12	067593
16	53	100.0	90	5	077091
17	53	100.0	96	6	077729
18	53	100.0	98	5	094162
19	53	100.0	101	5	090341

20	53	100.0	104	5	09NLE3	09nle3 leishmania
21	53	100.0	105	5	09NMV2	09nmv2 leishmania
22	53	100.0	108	5	09VUN1	09vun1 drosophila
23	53	100.0	110	4	014633	014633 homo sapien
24	53	100.0	115	5	046202	046202 drosophila
25	53	100.0	117	4	095176	095176 homo sapien
26	53	100.0	118	11	002393	002393 mus musculu
27	53	100.0	121	6	09RTG9	09rtg9 hylobates m
28	53	100.0	125	4	09S177	09s177 homo sapien
29	53	100.0	125	5	09N327	09n327 caenorhabdi
30	53	100.0	131	5	09M3A7	09m3a7 drosophila
31	53	100.0	135	5	018158	018158 caenorhabdi
32	53	100.0	137	5	018157	018157 caenorhabdi
33	53	100.0	137	6	09RTG8	09rtg8 hylobates a
34	53	100.0	137	6	09RTG7	09rtg7 hylobates k
35	53	100.0	137	6	09RTG6	09rtg6 hylobates m
36	53	100.0	142	5	09RTU5	09rtu5 caenorhabdi
37	53	100.0	144	6	077494	077494 tarsius ban
38	53	100.0	151	6	028576	028576 ovis aries
39	53	100.0	151	5	09XVX3	09xvx3 caenorhabdi
40	53	100.0	152	6	09RTU2	09rtu2 hylobates a
41	53	100.0	153	6	09RTU1	09rtu1 hylobates m
42	53	100.0	153	6	09RTU0	09rtu0 hylobates k
43	53	100.0	153	6	09RTG9	09rtg9 hylobates m
44	53	100.0	153	6	028834	028834 oryctolagus
45	53	100.0	154	12	084631	084631 paramacium

ALIGNMENTS

RESULT 1
077490 PRELIMINARY: PRT: 32 AA.

AC 077490;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE D4 DOPAMINE RECEPTOR (D4DR) (FRAGMENT).
OS Galago crassicaudatus (Thick-tailed galago) (Otollemur crassicaudatus).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Placentalia; Strepsirrhini; Galagonidae; Otollemur.
OX NCBI_TaxID=9463;
[1]
RP SEQUENCE FROM N.A.
RA Inoue-Murayama M., Takenaka O., Murayama Y.;
RT "Origin and divergence of tandem repeats of primate D4 dopamine
RT receptor genes.";
RL Primates 39:217-224(1998).
DR EMBL; AB016199; BAA32037.1; -.
FT NON_TER 1 32
FT NON_TER 32 32
SQ SEQUENCE 32 AA; 3157 MW; F4926F29C2C5CEC CRC64;

Query Match 100.0%; Score 53; DB 6; Length 32;
Best local Similarity 19.0%; Pred. No. 61;
Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXCXXC 21
DB 10 CDBDCEPPAPAGPSQDCDDPC 30
RESULT 2
077493 PRELIMINARY: PRT: 32 AA.
AC 077493;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE D4 DOPAMINE RECEPTOR (D4DR) (FRAGMENT).
OS Lemur catta (Ring-tailed lemur).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsitini; Lemuridae; Lemur.
 OX NCBI_TaxID=9447;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Inoue-Murayama M., Takenaka O., Murayama Y.;
 RT "Origin and divergence of tandem repeats of primate D4 dopamine
 receptor genes";
 RL Primates 39:217-224(1998).
 DR EMBL; AB016202; BAA32040.1; -.
 FT NON_TER 1
 FT NON_TER 32
 SQ SEQUENCE 32 AA; 3023 MW; F46F7D481DAF917C CRC64;

Query Match 100.0%; Score 53; DB 6; Length 32;
 Best Local Similarity 19.0%; Pred. No. 61;
 Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXCXXXXXXXXXXCXXC 21
 DB 10 CGADCOPAPGLPGCGPCDC 30

RESULT 3

ID Q16861 PRELIMINARY; PRT; 46 AA.
 AC Q16861;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, last annotation update)
 DE CYSTEINE-RICH PROTEIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lemasson I., Devaux C., Mesnard J.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63332; AAB05810.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 46 AA; 5061 MW; 311922FE40A44E8F CRC64;

Query Match 100.0%; Score 53; DB 4; Length 46;
 Best Local Similarity 19.0%; Pred. No. 75;
 Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXCXXXXXXXXXXCXXC 21
 DB 11 CCCCCCCCCCCCCCCCCC 31

RESULT 4

ID Q90623 PRELIMINARY; PRT; 58 AA.
 AC Q90623;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE METALLOTHIONEIN.
 OS Pacifastacus leniusculus (Signal crayfish).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Astacoidae; Astacidae; Pacifastacus.
 OX NCBI_TaxID=6720;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=THORACIC GANGLIA;
 RA Skorupski P., Dawbarn D.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF199482; AAF07215.1; -.

DR HSP; P55949; IDMC.
 DR INTERPRO; IPR002045; -.
 DR INTERPRO; IPR003019; -.
 DR PFAM; PF00131; metalchio.1.
 DR PRINTS; PR00858; MTCRUSTACEAN.
 SQ SEQUENCE 58 AA; 6008 MW; 576635ACB0E5100 CRC64;

Query Match 100.0%; Score 53; DB 5; Length 58;
 Best Local Similarity 19.0%; Pred. No. 86;
 Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXCXXXXXXXXXXCXXC 21
 DB 34 CTSCKCKPSKECAKTSKPC 54

RESULT 5

ID Q9M402 PRELIMINARY; PRT; 62 AA.
 AC Q9M402;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE ALPHA-TYPE BETA-CONGLICININ (FRAGMENT).
 GN BCSP.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Fabales; Fabaceae; Papilionoideae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Morasutti C., Marchetti S., De Amicis F., Zaina G., Zanetti M.;
 RT "Expression and purification of the antimicrobial peptide SMAP-29 from
 tobacco transgenic plants by ScvMA-intein system";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA De Amicis F.;
 RL Thesis (1998), University of Udine, DPTVA.
 DR EMBL; AJ276118; CAB83040.1; -.
 FT NON_TER 62
 FT NON_TER 62
 SQ SEQUENCE 62 AA; 7158 MW; 10690D53F7700443 CRC64;

Query Match 100.0%; Score 53; DB 10; Length 62;
 Best Local Similarity 19.0%; Pred. No. 89;
 Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXCXXXXXXXXXXCXXC 21
 DB 38 CLOSCSERDSYRNQACHARC 58

RESULT 6

ID Q41097 PRELIMINARY; PRT; 66 AA.
 AC Q41097;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)
 DE A615R PROTEIN.
 GN A615R.
 OS Paramesidium bursaria chlorella virus 1 (BCV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
 OX NCBI_TaxID=10506;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98022962; PubMed=9356347;
 RA Li Y., Lu Z., Sun L., Ropp S., Kutish G.F., Rock D.L., Van Etten J.L.;
 RT "Analysis of 74 kb of DNA located at the right end of the 330-kb
 chlorella virus BCV-1 genome.";

